

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/467,605

DATE: 12/18/96

TIME: 11:47:04

INPUT SET: S14460.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Pietropaolo, Massimo and Eisenbarth, George S.
6
7 (ii) TITLE OF INVENTION: Antigen Associated with Type I Diabetes Mellitus
8
9 (iii) NUMBER OF SEQUENCES: 2
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: LAHIVE & COCKFIELD
13 (B) STREET: 60 State Street, suite 510
14 (C) CITY: Boston
15 (D) STATE: Massachusetts
16 (E) COUNTRY: USA
17 (F) ZIP: 02109-1875
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Floppy disk
21 (B) COMPUTER: IBM PC compatible
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: 08/467,605
27 (B) FILING DATE: 06 June 1995
28 (C) CLASSIFICATION:
29
30 (vii) PRIOR APPLICATION DATA:
31 (A) APPLICATION NUMBER: 07/788,118
32 (B) FILING DATE: 01 November 1991
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Silveri, Jean M.
36 (B) REGISTRATION NUMBER: 39,030
37 (C) REFERENCE/DOCKET NUMBER: IMI-001CPDV
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (617)227-7400
41 (B) TELEFAX: (617)227-5941
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

18E 1813
Scheiner

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/467,605

DATE: 12/18/96

TIME: 11:47:07

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47 (A) LENGTH: 1785 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51

52 (ii) MOLECULE TYPE: cDNA
53
54

55 (ix) FEATURE:

56 (A) NAME/KEY: CDS
57 (B) LOCATION: 179..1628
58
59

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

61
62 CGGGCGGGGG ATACCCAGG AGATGGGGGT CGAGGAGAGA CCCCAGGGAG TAGAGAGAGA 60
63
64 GAAACTCACT CCCCAGTCC CCGACCCTCC CCAAGCAAGG TTATAATATA ACTTATCCTC 120
65
66 TCATGCTTTT TTCCTGCCCC TTCTCCCCAA ATCATCAACA ATAGAAGAAG AAGAAAAAC 178
67
68 ATG TCA GGA CAC AAA TGC AGT TAT CCC TGG GAC TTA CAG GAT CGA TAT 226
69 Met Ser Gly His Lys Cys Ser Tyr Pro Trp Asp Leu Gln Asp Arg Tyr
70 1 5 10 15
71
72 GCT CAA GAT AAG TCA GTT GTA AAT AAG ATG CAA CAG AGA TAT TGG GAG 274
73 Ala Gln Asp Lys Ser Val Val Asn Lys Met Gln Gln Arg Tyr Trp Glu
74 20 25 30
75
76 ACG AAG CAG GCC TTT ATT AAA GCC ACA GGG AAG AAG GAA GAT GAA CAT 322
77 Thr Lys Gln Ala Phe Ile Lys Ala Thr Gly Lys Lys Glu Asp Glu His
78 35 40 45
79
80 GTT GTT GCC TCT GAC GCG GAC CTG GAT GCC AAG CTA GAG CTG TTT CAT 370
81 Val Val Ala Ser Asp Ala Asp Leu Asp Ala Lys Leu Glu Leu Phe His
82 50 55 60
83
84 TCA ATT CAG AGA ACC TGT CTG GAC TTA TCG AAA GCA ATT GTA CTC TAT 418
85 Ser Ile Gln Arg Thr Cys Leu Asp Leu Ser Lys Ala Ile Val Leu Tyr
86 65 70 75 80
87
88 CAA CAG AGG ATA TGT TTC TTG TCT CAA GAA GAA AAC GAA CTG GGA AAA 466
89 Gln Gln Arg Ile Cys Phe Leu Ser Gln Glu Glu Asn Glu Leu Gly Lys
90 85 90 95
91
92 TTT CTT CGA TCC CAA GGT TTC CAA GAT AAA ACC AGA GCA GGA AAG ATG 514
93 Phe Leu Arg Ser Gln Gly Phe Gln Asp Lys Thr Arg Ala Gly Lys Met
94 100 105 110
95
96 ATG CAA GCG ACA GGA AAG GCC CTC TGC TTT TCT TCC CAG CAA AGG TTG 562
97 Met Gln Ala Thr Gly Lys Ala Leu Cys Phe Ser Ser Gln Gln Arg Leu
98 115 120 125
99

RAW SEQUENCE LISTING PATENT APPLICATION *US/08/467,605*

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100	GCC TTA CGA AAT CCT TTG TGT CGA TTT CAC CAA GAA GTG GAG ACT TTT	610
101	Ala Leu Arg Asn Pro Leu Cys Arg Phe His Gln Glu Val Glu Thr Phe	
102	130 135 140	
103		
104	CGG CAT CGG GCC ATC TCA GAT ACT TGG CTG ACG GTG AAC CGC ATG GAA	658
105	Arg His Arg Ala Ile Ser Asp Thr Trp Leu Thr Val Asn Arg Met Glu	
106	145 150 155 160	
107		
108	CAG TGC AGG ACG GAA TAT AGA GGA GCA CTA TTA TGG ATG AAG GAC GTG	706
109	Gln Cys Arg Thr Glu Tyr Arg Gly Ala Leu Leu Trp Met Lys Asp Val	
110	165 170 175	
111		
112	TCT CAG GAG CTT GAT CCA GAC CTC TAC AAG CAA ATG GAG AAG TTC AGG	754
113	Ser Gln Glu Leu Asp Pro Asp Leu Tyr Lys Gln Met Glu Lys Phe Arg	
114	180 185 190	
115		
116	AAG GTG CAA ACA CAA GTG CGC CTT GCA AAA AAA AAC TTT GAC AAA TTG	802
117	Lys Val Gln Thr Gln Val Arg Leu Ala Lys Lys Asn Phe Asp Lys Leu	
118	195 200 205	
119		
120	AAG ATG GAT GTG TGT CAA AAA GTG GAT CTT CTT GGA GCG AGC AGA TGC	850
121	Lys Met Asp Val Cys Gln Lys Val Asp Leu Leu Gly Ala Ser Arg Cys	
122	210 215 220	
123		
124	AAT CTC TTG TCT CAC ATG CTA GCA ACA TAC CAG ACC ACT CTG CTT CAT	898
125	Asn Leu Leu Ser His Met Leu Ala Thr Tyr Gln Thr Thr Leu Leu His	
126	225 230 235 240	
127		
128	TTT TGG GAG AAA ACT TCT CAC ACT ATG GCA GCC ATC CAT GAG AGT TTC	946
129	Phe Trp Glu Lys Thr Ser His Thr Met Ala Ala Ile His Glu Ser Phe	
130	245 250 255	
131		
132	AAA GGT TAT CAA CCA TAT GAA TTT ACT ACT TTA AAG AGC TTA CAA GAC	994
133	Lys Gly Tyr Gln Pro Tyr Glu Phe Thr Thr Leu Lys Ser Leu Gln Asp	
134	260 265 270	
135		
136	CCT ATG AAA AAA TTA GTT GAG AAA GAA GAG AAG AAG AAA ATC AAC CAG	1042
137	Pro Met Lys Lys Leu Val Glu Lys Glu Glu Lys Lys Lys Ile Asn Gln	
138	275 280 285	
139		
140	CAG GAA AGT ACA GAT GCA GCC GTG CAG CAG CCG AGC CAA TTA ATT TCA	1090
141	Gln Glu Ser Thr Asp Ala Ala Val Gln Gln Pro Ser Gln Leu Ile Ser	
142	290 295 300	
143		
144	TTA GAG GAA GAA AAC CAG CGC AAG GAA TCC TCT AGT TTT AAG ACT GAA	1138
145	Leu Glu Glu Glu Asn Gln Arg Lys Glu Ser Ser Ser Phe Lys Thr Glu	
146	305 310 315 320	
147		
148	GAT GGA AAA AGT ATT TTA TCT GCC TTA GAC AAA GGC TCT ACA CAT ACT	1186
149	Asp Gly Lys Ser Ile Leu Ser Ala Leu Asp Lys Gly Ser Thr His Thr	
150	325 330 335	
151		
152	GCA TGC TCA GGA CCC ATA GAT GAA CTA TTA GAC ATG AAA TCT GAG GAA	1234

RAW SEQUENCE LISTING PATENT APPLICATION US/98/467,605

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153	Ala Cys Ser Gly Pro Ile Asp Glu Leu Leu Asp Met Lys Ser Glu Glu	
154	340 345 350	
155		
156	GGT GCT TGC CTG GGA CCA GTG GCA GGG ACC CCG GAA CCT GAA GGT GCT	1282
157	Gly Ala Cys Leu Gly Pro Val Ala Gly Thr Pro Glu Pro Glu Gly Ala	
158	355 360 365	
159		
160	GAC AAA GAT GAC CTG CTG CTG TTG AGT GAG ATC TTC AAT GCT TCC TCC	1330
161	Asp Lys Asp Asp Leu Leu Leu Leu Ser Glu Ile Phe Asn Ala Ser Ser	
162	370 375 380	
163		
164	TTG GAA GAG GGC GAG TTC AGC AAA GAG TGG GCC GCT GTG TTT GGA GAC	1378
165	Leu Glu Glu Gly Glu Phe Ser Lys Glu Trp Ala Ala Val Phe Gly Asp	
166	385 390 395 400	
167		
168	GGC CAA GTG AAG GAG CCA GTG CCC ACT ATG GCC CTG GGA GAG CCA GAC	1426
169	Gly Gln Val Lys Glu Pro Val Pro Thr Met Ala Leu Gly Glu Pro Asp	
170	405 410 415	
171		
172	CCC AAG GCC CAG ACA GGC TCA GGT TTC CTT CCT TCG CAG CTT TTA GAC	1474
173	Pro Lys Ala Gln Thr Gly Ser Gly Phe Leu Pro Ser Gln Leu Leu Asp	
174	420 425 430	
175		
176	CAA AAT ATG AAA GAC TTA CAG GCC TCG CTA CAA GAA CCT GCT AAG GCT	1522
177	Gln Asn Met Lys Asp Leu Gln Ala Ser Leu Gln Glu Pro Ala Lys Ala	
178	435 440 445	
179		
180	GCC TCA GAC CTG ACT GCC TGG TTC AGC CTC TTC GCT GAC CTC GAC CCA	1570
181	Ala Ser Asp Leu Thr Ala Trp Phe Ser Leu Phe Ala Asp Leu Asp Pro	
182	450 455 460	
183		
184	CTC TCA AAT CCT GAT GCT GTT GGG AAA ACC GAT AAA GAA CAC GAA TTG	1618
185	Leu Ser Asn Pro Asp Ala Val Gly Lys Thr Asp Lys Glu His Glu Leu	
186	465 470 475 480	
187		
188	CTC AAT GCA TGA ATCTGTAC CCTTCGGAGG GCACTCACAT GCCGCCCCCA	1668
189	Leu Asn Ala *	
190		
191		
192	GCAGCTCCCC TGGGGGCTAG CAGAAGTATA AAGTGATCAG TATGCTGTTT TAATAATTAT	1728
193		
194	GTGCCATTTT AATAAAATGA AAGGGTCAAC GGCCCTGTTA AAAAAAAAAA AAAAAAA	1785
195		
196		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

INPUT SET: S14460.raw

206	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:																
207																	
208	Met	Ser	Gly	His	Lys	Cys	Ser	Tyr	Pro	Trp	Asp	Leu	Gln	Asp	Arg	Tyr	
209	1				5					10					15		
210																	
211	Ala	Gln	Asp	Lys	Ser	Val	Val	Asn	Lys	Met	Gln	Gln	Arg	Tyr	Trp	Glu	
212				20					25					30			
213																	
214	Thr	Lys	Gln	Ala	Phe	Ile	Lys	Ala	Thr	Gly	Lys	Lys	Glu	Asp	Glu	His	
215			35					40					45				
216																	
217	Val	Val	Ala	Ser	Asp	Ala	Asp	Leu	Asp	Ala	Lys	Leu	Glu	Leu	Phe	His	
218		50					55					60					
219																	
220	Ser	Ile	Gln	Arg	Thr	Cys	Leu	Asp	Leu	Ser	Lys	Ala	Ile	Val	Leu	Tyr	
221	65					70					75					80	
222																	
223	Gln	Gln	Arg	Ile	Cys	Phe	Leu	Ser	Gln	Glu	Glu	Asn	Glu	Leu	Gly	Lys	
224					85					90					95		
225																	
226	Phe	Leu	Arg	Ser	Gln	Gly	Phe	Gln	Asp	Lys	Thr	Arg	Ala	Gly	Lys	Met	
227				100					105					110			
228																	
229	Met	Gln	Ala	Thr	Gly	Lys	Ala	Leu	Cys	Phe	Ser	Ser	Gln	Gln	Arg	Leu	
230			115					120					125				
231																	
232	Ala	Leu	Arg	Asn	Pro	Leu	Cys	Arg	Phe	His	Gln	Glu	Val	Glu	Thr	Phe	
233		130					135					140					
234																	
235	Arg	His	Arg	Ala	Ile	Ser	Asp	Thr	Trp	Leu	Thr	Val	Asn	Arg	Met	Glu	
236	145					150					155					160	
237																	
238	Gln	Cys	Arg	Thr	Glu	Tyr	Arg	Gly	Ala	Leu	Leu	Trp	Met	Lys	Asp	Val	
239					165					170					175		
240																	
241	Ser	Gln	Glu	Leu	Asp	Pro	Asp	Leu	Tyr	Lys	Gln	Met	Glu	Lys	Phe	Arg	
242				180					185					190			
243																	
244	Lys	Val	Gln	Thr	Gln	Val	Arg	Leu	Ala	Lys	Lys	Asn	Phe	Asp	Lys	Leu	
245			195					200					205				
246																	
247	Lys	Met	Asp	Val	Cys	Gln	Lys	Val	Asp	Leu	Leu	Gly	Ala	Ser	Arg	Cys	
248		210															